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 Show: ☐ 1: NM_074070. Caenorhabditis el...[gi:17563083]

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LOCUS 50445Co 738 bp mRNA linear INV 22-NOV-2002
DEFINITION Caenorhabditis elegans GYF domain containing protein (27.5 kD),
alternative variant d, mRNA.
ACCESSION NM_074070
VERSION NM_074070.1 GI:17563083
KEYWORDS .
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
COMMENT VALIDATED REFSEQ: This record has undergone preliminary review of
the sequence, but has not yet been subject to final NCBI review.
The reference sequence was derived from WormBase CDS:R10D12.14.
Fully supported by cDNA from the Worm Transcriptome Project.
COMPLETENESS: full length.
FEATURES
source Location/Qualifiers
1..738
/organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/chromosome="V"
/map="V;+5.72 cM (interpolated genetic position)"
/map="V; covering 3369 bp, from base 13965013 to 13968383
on genome release WS85"
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ATGCACAAGAACGGAAACAATGGA (T=58.5),
TTAGTTGATGATAACCATTTGTCCGAG (T=59.0)"
/clone_lib="[Predicted cellular localisation] PSORT II
analysis, (K. Nakai) trained on yeast data predicts that
the subcellular location of this protein is most likely in
the nucleus (56%). Less likely possibilities are in the
cytoplasm (26%) or in the cytoskeleton (13%) or in the
mitochondria (4%)."
gene 1..738
/gene="50445Co"
/note="50445; synonyms: R10D12.13a, R10D12.13b,
R10D12.13c, R10D12.14, CELK02289"
CDS 1..738
/gene="50445Co"
/note="|| [Common ancestor, from TaxBlast with threshold
10-3] Fungi Metazoa group || [Closest homologs]
Schizosaccharomyces pombe: ref|NP 594756.1| (score=45);
Caenorhabditis elegans: ref|NP 506471.1| (422); Drosophila
melanogaster: gb|AAF59406.1| (46); Mus musculus: ref|NP
113596.1| (49); Homo sapiens: dbj|BAA91873.1| (50)"
/codon_start=1
/product="GYF domain containing protein (27.5 kD)"
/protein_id="NP_506471.1"

h cb hg e e e fcg c e e e b c e e

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/db_xref="LocusID:179891"
/db_xref="NextDB:CELK02289"
/db_xref="Worfdb:R10D12.13a"
/db_xref="WormBase:R10D12.13a"
/db_xref="WormBase:R10D12.13b"
/db_xref="WormBase:R10D12.13c"
/db_xref="WormBase:R10D12.14"
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NQFQPPMPMRFPFPLPMPLLHQMNNQNGPPMGAQMHSQPPSEPIDAGSLSHTPDSENET
RLNEQTLQQPPSWLIALGLAGHGRKPHHHQQILAHQHQPQMQHANVATDQVVMKSVEC
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misc feature
37..204
/gene="50445Co"
/note="Region: [Pfam/InterPro description] GYF domain: the
GYF domain is named because of the presence of Gly-Tyr-Phe
residues. The GYF domain is a proline-binding domain in
CD2-binding protein O95400. HMMER score 38.20
Evalue=1.2e-08"
/db_xref="CDD:pfam02213"
BASE COUNT      211 a      204 c      159 g      164 t
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  61 gacagtgaata aatatggacc atatatgtca aaggatatgc tgttctggct tcaagcggga
 121 tacttcaacg acggtctcca attgaaaact gaaaatgagc caaactatca tacgcttgga
 181 gaggaggagcc aattgctcgg aactcaccca ttcagtatgc ctgtgcactc actggatgag
 241 acgattgctc agatgaactc aatgcggcct cacggagcaa tgatgatggt tccacctgga
 301 cttcaaaatc aattccaacc accgatgccg atgcgtttcc caccattcct tccaatgccg
 361 cttctccatc aaatgaatca aaatggacca ccaatgggtg ctcaaataca ttctcagcca
 421 ccatcgagagc caatcgagcg tggatctctg tcccatatcc cagattccga gaacgaaacg
 481 cggttaaacg agcaaaactc ccagcagcct ccatcggtgg taattgccct tggcctggcg
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 721 atggttatca tcaactaa
//
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Revised: July 5, 2002.

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Jan 21 2003 18:08:12

h cb hg e e e fcg c e e e b ce e